NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: ___SEE ENCLOSED NOTE___

Applicant Must Provide:

☒ An _initial_ or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An _initial_ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/881,509B*

DATE: 09/10/1999
TIME: 09:50:19

Schwadron

1644 RUSH #12

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> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

ENTERED

```
 1                              SEQUENCE LISTING
 2
 3   (1)      General Information:
 4
 5       (i)  APPLICANT:   SCHENDEL, Dolores J.
 6
 7      (ii)  TITLE OF INVENTION:  T CELLS SPECIFIC FOR KIDNEY CARCINOMA
 8
 9     (iii)  NUMBER OF SEQUENCES: 44
10
11      (iv)  CORRESPONDENCE ADDRESS:
12           (A)   ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
13           (B)   STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
14           (C)   CITY: Washington
15           (D)   STATE: DC
16           (E)   COUNTRY: USA
17           (F)   ZIP: 20005-5701
18
19       (v)  COMPUTER READABLE FORM:
20           (A)   MEDIUM TYPE: Floppy disk
21           (B)   COMPUTER: IBM PC compatible
22           (C)   OPERATING SYSTEM: PC-DOS/MS-DOS
23           (D)   SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25      (vi)  CURRENT APPLICATION DATA:
26           (A)   APPLICATION NUMBER: 08/881,509
27           (B)   FILING DATE: June 24, 1997
28           (C)   CLASSIFICATION:
29
30    (viii)  ATTORNEY/AGENT INFORMATION:
31           (A)   NAME: Kitts, Monica Chin
32           (B)   REGISTRATION NUMBER: 36,105
33           (C)   REFERENCE/DOCKET NUMBER: 564-7015
34
35      (ix)  TELECOMMUNICATION INFORMATION:
36           (A)   TELEPHONE: (202) 638-5000
37           (B)   TELEFAX: (202) 638-4810
38
39
40   (2) INFORMATION FOR SEQ ID NO: 1:
41
42   (i) SEQUENCE CHARACTERISTICS:
43           (A) LENGTH: 1341 base pairs
44           (B) TYPE: nucleic acid
45           (C) STRANDEDNESS: both
46           (D) TOPOLOGY: linear
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47
48          (ix)  FEATURE:
49               (A)  NAME/KEY: CDS
50               (B)  LOCATION:1..801
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52          (ix)  FEATURE:
53               (A)  NAME/KEY: sig_peptide
54               (B)  LOCATION:1..54
55
56          (ix)  FEATURE:
57               (A)  NAME/KEY: mat_peptide
58               (B)  LOCATION:55..801
59
60          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61
62     ATG AGG CAA GTG GCG AGA GTG ATC GTG TTC CTG ACC CTG AGT ACT TTG            48
63     Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
64     -18         -15                 -10                 -5
65
66     AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA            96
67     Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
68              1               5                 10
69
70     CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT           144
71     Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
72      15                  20                  25                  30
73
74     TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT           192
75     Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
76                      35                  40                  45
77
78     ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT           240
79     Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
80                  50                  55                  60
81
82     ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC           288
83     Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
84              65                  70                  75
85
86     CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG           336
87     Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
88              80                  85                  90
89
90     CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC           384
91     Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
92      95                  100                 105                 110
93
94     CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT           432
95     Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
96                      115                 120                 125
97
98     GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG           480
99     Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
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102    TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA        528
103    Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
104        145              150              155
105
106    GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC        576
107    Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
108        160              165              170
109
110    AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT        624
111    Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
112        175              180              185              190
113
114    CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG        672
115    Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
116                 195              200              205
117
118    CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC        720
119    Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
120                 210              215              220
121
122    CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT        768
123    Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
124            225              230              235
125
126    AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA      821
127    Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
128        240              245
129
130    GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG      881
131
132    AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA      941
133
134    ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA     1001
135
136    CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA     1061
137
138    GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC     1121
139
140    CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCCTGGAG     1181
141
142    AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTCATA AAGAAATACA TAGTATTCTT     1241
143
144    CTTCTCAAGA CGTGGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG     1301
145
146    GGCGTGTTGT ATGTCCTGCT GCCGATGCCT TCATTAAAAT                           1341
147
148
149    (2) INFORMATION FOR SEQ ID NO: 2:
150
151    (i) SEQUENCE CHARACTERISTICS:
152            (A) LENGTH: 267 amino acids
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153          (B)  TYPE: amino acid
154          (D)  TOPOLOGY: linear
155
156      (ii)  MOLECULE TYPE: protein
157
158      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
159
160   Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
161   -18          -15              -10                  -5
162
163   Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
164            1           5                  10
165
166   Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
167    15              20               25                      30
168
169   Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
170            35              40                      45
171
172   Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
173            50              55                  60
174
175   Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
176        65              70                  75
177
178   Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
179        80              85                  90
180
181   Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
182    95              100             105                     110
183
184   Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
185              115             120                     125
186
187   Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
188            130             135                     140
189
190   Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
191        145             150                     155
192
193   Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
194        160             165                     170
195
196   Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
197    175             180                 185                     190
198
199   Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
200              195             200                     205
201
202   Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
203            210             215                     220
204
205   Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
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206              225              230              235
207
208  Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
209       240              245
210
211
212  (2) INFORMATION FOR SEQ ID NO: 3:
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214  (i) SEQUENCE CHARACTERISTICS:
215          (A)  LENGTH: 936 base pairs
216          (B)  TYPE: nucleic acid
217          (C)  STRANDEDNESS: both
218          (D)  TOPOLOGY: linear
219
220      (ix)  FEATURE:
221          (A)  NAME/KEY: CDS
222          (B)  LOCATION:1..933
223
224      (ix)  FEATURE:
225          (A)  NAME/KEY: sig_peptide
226          (B)  LOCATION:1..63
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228      (ix)  FEATURE:
229          (A)  NAME/KEY: mat_peptide
230          (B)  LOCATION:64..933
231
232      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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235  Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
236  -21 -20              -15              -10
237
238  GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA        96
239  Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
240   -5               1               5                    10
241
242  CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC       144
243  Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
244              15              20              25.
245
246  TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT       192
247  Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
248          30              35              40
249
250  CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC       240
251  Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
252          45              50              55
253
254  GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG       288
255  Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
256   60              65              70              75
257
258  AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC       336
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/881,509B*

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